

SEQUENCE LISTING

<110> WINDSOR-HINES, Dawn

RAO, Patricia

RINGLER, Douglas J.

<120> INDUCING TOLERANCE IN PRIMATES

<130> TLN-022

<150> 60/431839

<151> 2002-12-09

<160> 70

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(717)

<400> 1

atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48
Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Trp Val Pro
1 5 10 15

ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45

gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60

gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80

ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys

100 105 110
cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val
115 120 125

gaa atc aaa cga act gtg gct gca cca tct gtc atc ttc ccg cca 432
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

aag gac agc acc tac agc ctc agc acc ctg acg ctg agc aaa gca 624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
225 230 235

<210> 2
<211> 716
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 2
atggagacag acacaatccct gctatgggtg ctgctgcctt gggttccagg ctccactgg 60
gacattgtga tgacccaatc tccagattct ttggctgtgt ctcttaggtga gagggccacc 120
atcaactgca aggcacgcca aagtgttgc tatgtatggt atagttatat gaactggat 180
caacagaaac caggacacgac accccaaactc ctcatctatg ttgcatccaa tctagaggct 240
ggggtcccaag acagggttag tggcagtggg tctgggacag acttcaccct caccatcgt 300
tctctgcagg cggaggatgt tgcaagtctat tactgtcagc aaagtctca ggaccctccg 360
acgttcgggtg gaggtaccaa ggtggaaatc aaacgaactg tggctgcacc atctgtctc 420
atctcccgcc catctgtga gcagttgaaa tctggaactg cctctgtgt gtgcctgtg 480
ataaactct atcccagaga ggccaaagta cagtggaaagg tggataacgc cctcaatcg 540
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 600
acaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgccc tgcgaagtca 660

cccatcaggc cctgagctcg cccgtcacaa agagctcaa caggggagag tgtag 716

<210> 3

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 3

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val
115 120 125
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 4

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 4

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
85 90 95
Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 5
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<221> CDS
<222> (1)...(1404)

<400> 5
atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48
Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
1 5 10 15

gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn

65 70 75 80

gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

aca gtc tac atg gaa ctc agc agc ctg agg tct gag gac act gcg gtc 336
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
115 120 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720
Lys Pro Ser Asn Thr Lys Val Asp Lys Val Glu Pro Lys Ser Cys
225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc gcg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly
245 250 255

gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

290 295 300

cat aat gcc aag aca aag ccg cggtt gag gag cag tac aac aac agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

cgt gtg gtc agc gtc ctc 'acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccg ggt aaa tga 1404
Pro Gly Lys *
465

<210> 6
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 6

atggaatgga tctggatctt ttccttcac tcgtcaggaa ctcgagggtgt ccagtcccg 60
gttcagctgg tcgagtctgg agctgaagtg aagaaggctg gggctcagt gaagggtgtcc 120
tgtaaaggctt ctggatacac attcaacttgc tatgttataa gctgggtgag gcaggcacct 180
ggacagggcc ttgagtgat gggagagat tatcctggaa gcggtatgtat ttattataat 240
gagaagttca agggcagggt cacaatgact agagacacat ccaccacac agtctacatg 300
gaactcagca gcctgaggctc tgaggacact gcggtctatt actgtgcaag atccggggac 360
ggcagtcgt tttttactg gggccaaggg acactatgtca cagtcctc caccctccacc 420
aaggcccat cggcttccc cctggcaccc tcctccaaga gacccctgg gggcacagcg 480
gccctgggt gcctggtaa ggactacttc cccgaaccgg tgacgggtgc gtggactca 540
ggcgcctgta ccagcggcgt gcacacettc cggcgtgtcc tacagtccctc aggactctac 600
tccctcagca gctgtgtac cgtgcctcc accgatgttgc gacccagac ctacatctgc 660
aacgtgaatc acaagccag caacaccaag gtggacaaga aagtgagcc caaatctgt 720
gacaaaactc acacatgccc accgtgcca gcacctgaac tcggggggc accgtcagtc 780
ttccttcc cccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840
tgcgtgggg tggacgtgag ccacgaagac cctggaggta agttcaactg gtacgtggac 900
ggcgtggagg tgcataatgc caagacaag cgcggggagg agcagtacaa cagcacgtac 960
cgtgtgtca cgtccctcac cgtctgcac caggactgg tgaatggca ggagttacaag 1020
tgcaaggtct ccaacaaage cctcccaagc cccatcgaga aaaccatctc caaagccaa 1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggatga gctgaccaag 1140
aaccaggtaa gcctgacccctg cctggtaaa ggcttctatc ccagcgacat cgccgtggag 1200
tgggagagca atggcagcc ggagacacaac tacaagacca cgcctccctg gctggaccc 1260
gacggctctt tcttccteta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1320
aacgtctct catgtccctg gatgtcatgag gctctgcaca accactacac gcagaagagc 1380
ctctccctgt ctccggtaa atga 1404

<210> 7

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 7

Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
1 5 10 15
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
115 120 125
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220
Lys Pro Ser Asn Thr Lys Val Asp Lys Val Glu Pro Lys Ser Cys
225 230 235 240
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly
245 250 255
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460
Pro Gly Lys
465

<210> 8
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 8
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30
Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe

50	55	60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr		
65	70	75
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr		
100	105	110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro		
115	120	125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly		
130	135	140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn		
145	150	155
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		
165	170	175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser		
180	185	190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser		
195	200	205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr		
210	215	220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser		
225	230	235
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg		
245	250	255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro		
260	265	270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala		
275	280	285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val		
290	295	300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr		
305	310	315
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr		
325	330	335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu		
340	345	350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys		
355	360	365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser		
370	375	380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp		
385	390	395
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser		
405	410	415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala		
420	425	430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
435	440	445

<210> 9
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(717)

<400> 9

atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48
Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45

gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60

gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80

ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110

cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val
115 120 125

gaa atc aaa cga act gtg gct gca cta tct gtc ttc atc ttc ccg cca 432
Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca 624

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
225 230 235

<210> 10

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 10

atggagacag acacaatctt gctatgggtg ctgctgtctt gggttccagg ctccactgg 60
gacattgtgtg tgacccaatc tccagattttt ttggctgtgt ctcttaggtga gaggccacc 120
atcaactgca agggcagccaa aagtgtttagt tatgtatggt atagttatataa gaactggat 180
caacagaaac caggacagcc accccaaactc ctcatctatg ttgcacccaa tctagaggct 240
ggggtcccaag acagggttagg tggcagtggg tctgggacag acttcaccctt caccatcgt 300
tctctgcagg cggaggatgt tgcatgttat tactgtcagc aaagtcttca ggaccctccg 360
acgttcggtg gaggtaaaaaa ggtggaaatc aaacgaactg tggctgcact atctgttttc 420
atcttcccgcc catctgtatc gcatgttggaaa tctggaaactg cctctgttgtt gtgcctgtg 480
aataacttctt atcccaagaga ggccaaatgtt cagtgaaagg tggataacgc cctccaaatcg 540
ggttaactccc aggagatgtt cacagagcag gacagcaagg acagcaccta cagectcagg 600
agcaccctgtg cgcttgacaa agcagactac gagaacaca aagtctacgc ctgcgaatgc 660
acccatcagg gcctgagtc gcccgtcaca aagagcttca acaggggaga gtgttag 717

<210> 11

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 11

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
115 120 125
Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
130 135 140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 12
<211> 218
<212> PRT
<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 12
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
85 90 95
Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 13
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<221> CDS
<222> (1)...(1404)

<400> 13
atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48
Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
1 5 10 15

gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtt aag aag 96
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
65 70 75 80

gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

aca gtc tac atg gaa ctc agc ctg agg tct gag gac act ggc gtc 336
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384
Tyr Tyr Cys Ala Arg Ser Gly Ser Arg Phe Val Tyr Trp Gly
115 120 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

165 170 175

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala

180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aac gtt gag ccc aaa tct tgt 720
Lys Pro Ser Asn Thr Lys Val Asp Lys Val Glu Pro Lys Ser Cys
225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccg ccg gag gag cag tac gcc agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
305 310 315 320

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acg aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccg ggt aaa tga 1404
Pro Gly Lys *
465

<210> 14
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

ctctccctgt ctccggtaa atga 1404

<210> 15

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 15

Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly

1 5 10 15

Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35 40 45

Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

50 55 60

Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn

65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser

85 90 95

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val

100 105 110

Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly

115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala

145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala

180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His

210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His

275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr

305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

355 360 365
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460
Pro Gly Lys
465

<210> 16
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 16
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30
Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140
Cys Leu Val Lys Asp Tyr Phe Pro Val Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val
290 295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 17

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(717)

<400> 17

atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48
Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45

gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60

gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80

ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110

cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val
115 120 125

gaa atc aaa cga act gtg gct gca cta tct gtc ttc atc ttc ccg cca 432
Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca 624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
225 230 235

<210> 18
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 18

atggagacag acacaatct gctatgggtg ctgctgtct gggttccagg ctccactgg 60
gacattgtga tgaccaatc tccagattct ttggctgtgt ctctaggtga gaggccacc 120
atcaactgca aggcagcca aagtgttgc tatgtgtgt atagttat gaactggat 180
caacagaaac caggacagcc acccaaactc ctcatctatg ttgcaccaa tctagagtct 240
ggggtcccg acagggttag tggcagtggg tctgggacag acttcaccc caccatcgt 300
tctctgcagg cggaggatgt tgcaagtctat tactgtcagc aaagtctca ggaccctccg 360
acgttcggtg gaggtacca ggtggaaatc aaacgaactg tggctgcact atctgtttc 420
atctcccgcatctgtac gcaatgttgc tctggaaactg cctctgtgt gtgcctgtg 480
aataactct atcccagaga ggc当地aaactg cagtgaaagg tggataacgc cctccaaatcg 540
gtaactccc aggagatgt cacagagcag gacagcaagg acagcacca cagcctcagc 600
agcacccctgacgctgagca agcagactac gagaacaca aagtctacgc ctgcgaagtc 660
acccatcagg gcctgagctc gcccgtcaca aagagctca acagggaga gtgttag 717

<210> 19

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 19

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val
115 120 125
Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
130 135 140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 20

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 20

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
85 90 95
Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 21

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(1404)

<400> 21

atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48
Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
1 5 10 15

gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96

Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
65 70 75 80

gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

aca gtc tac atg gaa ctc agc ctg agg tct gag gac act gcg gtc 336
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384
Tyr Tyr Cys Ala Arg Ser Gly Ser Arg Phe Val Tyr Trp Gly
115 120 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc gcg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly
245 250 255

gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccg ggt aaa tga 1404
Pro Gly Lys *
465

<210> 22
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 22
atggaatgga tctggatctt ttcctcatac ctgtcaggaa ctcgagggtgt ccagtccca 60
gttcagctgg tgcagtctgg agctgaagtg aagaaggctg gggctcagt gaagggtgtcc 120
tgttaaggctt ctggatacac attcaactgcc tatgttataa gctgggttag gcaggcacct 180
ggacagggcc ttgagtgat gggagagatt tatcctggaa gccgttagtag ttattataat 240
gagaagttca agggcagggt cacaatgact agagacacat ccaccacac agtctacatg 300
gaactcagca gctctgagggtc tgaggacact gccggcttatt actgtgcaag atccggggac 360
ggcagtcggt ttgttactg gggccaaggg acacttagtca cagtcctc acgcctccacc 420
aaggcccattt cggcttcctt cctggcaccc ttctccaaga gcacctctgg gggcacagcg 480
gcctctggctt gcctggtaaa ggactacttc cccgaaccgg tgacgggttc gtggactca 540
ggcgcccttga ccagcgggtt gcacacettc cccggctgtcc tacagtccctc aggactctac 600
ttccctcagca gctgtggtagc cgtgcctcc acgcagttgg gcacccagac ctacatctgc 660
aacgtgaatc acaagcccaag caacaccaag gtggacaaga aagtgtgacca acaaacttgt 720
gacaaaactc acacatgccc accgtgccccca gcacctgaac tcggggggcc accgtcagtc 780
ttcccttcc cccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840
tgcgtgggg tggacgttag ccacgaagac ctcgagggtca agttcaactg gtacgtggac 900
ggcgtgggg tgcataatgc caagacaag ccggggggagg agcagtacaa cagcacgtac 960
cgtgtggtca gctgcctcac cgtcctgcac caggacttgc tgaatggcaaa ggagtacaag 1020
tgcaagggtt ccaacaaacgc cctcccaagcc cccatcgaga aaaccatctc caaagccaaa 1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggatga gctgaccaag 1140
aaccagggtca gcctgacccctt cctggtaaaa ggcttctatc ccagcgtacat cggcgtggag 1200
tgggagagca atgggacgcc ggagaacaac tacaagacca cgcctcccggtt getggactcc 1260
gacggctctt tcttcctcta cagcaagctc accgtggaca agagcagggtg gcagcagggg 1320
aacgtctctt catgctcccgat gatgtcatgag gctctgcaca accactacac gcagaagagc 1380
ctctccctgtt ctccgggttaa atga 1404

<210> 23
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 23
Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
1 5 10 15
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser

85	90	95
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val		
100	105	110
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly		
115	120	125
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser		
130	135	140
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala		
145	150	155
160		
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val		
165	170	175
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala		
180	185	190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val		
195	200	205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His		
210	215	220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys		
225	230	235
240		
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly		
245	250	255
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met		
260	265	270
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His		
275	280	285
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val		
290	295	300
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr		
305	310	315
320		
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly		
325	330	335
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile		
340	345	350
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val		
355	360	365
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser		
370	375	380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu		
385	390	395
400		
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro		
405	410	415
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val		
420	425	430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met		
435	440	445
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser		
450	455	460
Pro Gly Lys		
465		

<210> 24
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 24

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
 20 25 30
 Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Ile Tyr Pro Gly Ser Gly Ser Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205
 Asn Thr Lys Val Asp Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 260 265 270
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 325 330 335
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 25
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<221> CDS
<222> (1)...(717)

<400> 25
atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48
Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45

gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60

gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80

ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

ctc acc atc agt tct ctg cag geg gag gat gtt gca gtc tat tac tgt 336
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110

cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val
115 120 125

gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca 432
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu

145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

aag gac agc acc tac agc ctc agc acc ctg acg ctg agc aaa gca 624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
225 230 235

<210> 26

<211> 716

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 26

atggagacag acacaatctt gctatgggtg ctgctgtctt gggttccagg ctccactgg 60
gacatgtgtatg tgacccaatc tccagattttt ttggctgtgt ctcttaggttga gaggccacc 120
atcaactgca aggccagcca aagtgttgc tatgtatggt atatgttatataa gaactggat 180
caacagaaac caggacagcc accccaaactc ctcatatgttgcattccaa tctagaggct 240
ggggtcccaag acagggttag tggcagtggg tctgggacag acttcacccctt caccatgtt 300
tctctgcagg cggaggatgt tgcagtttat tactgtcagc aaagtcttca ggaccctccg 360
acgttcgggtg gaggtaccaa ggtggaaatc aaacgaactg tggctgcacc atctgtcttc 420
atcttcccgcc catctgtatg gcagttggaaatc tctggaaactg cctctgttgtt gtgcctgtg 480
aataacttctt atcccaagaga ggcacaaatgtt cagttggagg tggataacgc cctccaaatcg 540
gttaactccc aggagatgtt cacagacgcg gacagcaagg acageaccta cagccctcagg 600
acaccctgac gctgagccaaatc gcagactacg agaaacacaa agtctacgccc tgcgaaatcg 660
cccatcagggtt cctgagctcg cccgttccaaatc agagtttcaatc caggggagatgtt 716

<210> 27

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 27

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Trp Val Pro

1 5 10 15
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val
115 120 125
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 28
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 28
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
85 90 95
Gln Asp Pro Pro Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 29
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<221> CDS
<222> (1)...(1404)

<400> 29
atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48
Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
1 5 10 15

gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
65 70 75 80

gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

aca gtc tac atg gaa ctc agc agc ctg agg tct gag gac act gcg gtc 336
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384
Tyr Tyr Cys Ala Arg Ser Gly Ser Arg Phe Val Tyr Trp Gly

115 120 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720
Lys Pro Ser Asn Thr Lys Val Asp Lys Val Glu Pro Lys Ser Cys
225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

gga ccg tca gtc ttc ctc tcc ccc cca aaa ccc aag gac acc ctc atg 816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc ccg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccg ccg gag gag cag tac gcc agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
305 310 315 320

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccg ggt aaa tga 1404
Pro Gly Lys *
465

<210> 30
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 30
atggaatgga tctggatctt tctccatc ctgtcaggaa ctcgagggtt ccagtcccg 60
gttcagctgg tgcagtctgg agctgaagtg aagaaggctg gggctcagt gaagggttcc 120
tgttaaggctt ctggatacac attcaacttccatgttataa gctgggttggag gcaggccacct 180
ggacaggggcc ttgagtgat gggagagatt tatcctggaa gcggttagtag ttattataat 240
gagaagtctca agggcagggtt cacaatgttca agagacacat ccaccacacat agtctacatg 300
gaactcagca gcctcagggtt tgaggacactt gcccgttattt actgttcaag atccggggac 360
ggcagtctgg ttgtttactt gggccaaagggg acactgttca cagtccttc agcccccacc 420
aaggggccat cggcttccc cctggcaccc ttctccaaga gcacccctgg gggcacagcg 480
gcccctggctt gcctggctaa ggactacttcc cccgaaccgg tgacgggttc gtggaaactca 540
ggcgccttgc ccagegggtt gcacacccctt cccgttccatgttca aggacttac 600
tccctcagca gctgtgggttgc cgtgccttcc agcagcttgg gcaccacagac ctacatctgc 660
aacgttcaatc acaagcccttca aacaccaaga aatgttggacca aatcttgc 720

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 780
ttcctcttcc ccccaaacc caaggacacc ctcatgaact cccggacccc tgaggtcaca 840
tgcgtgggg tggacgtgag ccacgaagac cctgagggtca agtcaactg gtacgtggac 900
ggcgtggagg tgcataatgc caagacaaag cggcggggagg agcagtacgc cagcacgtac 960
cgtgtggtca ggcgcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020
tgcaagggtc ccaacaaagc cctcccaagcc cccatcgaga aaaccatctc caaagccaa 1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag 1140
aaccagggtca gcctgacccctg cctggtcaaa ggcttctatc ccagcgacat cggcgtggag 1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc 1260
gacggctctt ctccctcta cagcaagctc acctggaca agageagggtg gcagcagggg 1320
aacgtctctc catgtccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380
ctctccctgt ctccggtaa atga 1404

<210> 31

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 31

Met	Glu	Trp	Ile	Trp	Ile	Phe	Leu	Leu	Ile	Leu	Ser	Gly	Thr	Arg	Gly
1	5			10					15						
Val	Gln	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
	20			25					30						
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
	35			40				45							
Thr	Ala	Tyr	Val	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
	50			55				60							
Glu	Trp	Met	Gly	Glu	Ile	Tyr	Pro	Gly	Ser	Ser	Tyr	Tyr	Asn		
	65			70			75		80						
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser
	85			90			95								
Thr	Val	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
	100			105				110							
Tyr	Tyr	Cys	Ala	Arg	Ser	Gly	Asp	Gly	Ser	Arg	Phe	Val	Tyr	Trp	Gly
	115			120			125								
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
	130			135			140								
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
	145			150			155		160						
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
	165			170			175								
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
	180			185			190								
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
	195			200			205								
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
	210			215			220								
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Val	Glu	Pro	Lys	Ser	Cys	
	225			230			235		240						
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Lys	
	245			250			255								
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
	260			265			270								

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
305 310 315 320
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460
Pro Gly Lys
465

<210> 32
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 32
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30
Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205
Asn Thr Lys Val Asp Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val
290 295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 33
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<221> CDS
<222> (1)...(1356)

<400> 33
cag gtt caa ttg gtg gag tct gga gga ggc gtt gta cag cct gga agg 48
Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tca tgt gca gct tct gga ttc act ttc agt gac ttt 96

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Phe
20 25 30

ggc atg aac tgg gtt cga cag gct ccc ggg aag ggg ctg gaa tgg gtg 144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca ctg att tac tat gat ggt agt aac aag ttc tat gca gac tct gtg 192
Ala Leu Ile Tyr Tyr Asp Gly Ser Asn Lys Phe Tyr Ala Asp Ser Val
50 55 60

aag ggt cga ttc acc atc tcc agg gac aat tct aag aac acc cta tac 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gca aaa ccc cac tat gat ggt tat tat cac ttc ttt gat tcc tgg ggc 336
Ala Lys Pro His Tyr Asp Gly Tyr Tyr His Phe Phe Asp Ser Trp Gly
100 105 110

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 384
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg 432
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 480
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 528
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 576
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 624
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 672
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg 720
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 768

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac 816
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 864
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 912
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 960
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1008
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1056
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1104
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1152
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1200
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg 1248
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1296
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct 1344
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

ccg ggt aaa tga 1356
Pro Gly Lys *
450

<210> 34
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<221> CDS
<222> (1)...(642)

<400> 34
gac atc cag atg acc cag agc cca agc agc ctg agc gcc agc gtg ggt 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

gac aga gtg acc atc acc tgt aaa gga agt cag gat att aac aat tac 96
Asp Arg Val Thr Ile Thr Cys Lys Gly Ser Gln Asp Ile Asn Asn Tyr
20 25 30

tta gcc tgg tac cag cag aag cca ggt aag gtc cca aag ctg ctg atc 144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile
35 40 45

tac aat aca gac att ttg cac acg ggt gtg cca agc aga ttc agc ggt 192
Tyr Asn Thr Asp Ile Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag cca 240
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

gag gac atc gcc acc tac tac tgc tat cag tat aac aac ggg tac acg 288
Glu Asp Ile Ala Thr Tyr Tyr Cys Tyr Gln Tyr Asn Asn Gly Tyr Thr
85 90 95

ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca cca 336
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act 384
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa 432
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag 480
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

agt gtc aca gag cag gac aag gac agc acc tac agc ctc agc agc 528
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc 576
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc 624
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

aac agg gga gag tgt tag 642
Asn Arg Gly Glu Cys *
210

<210> 35
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 35
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45
Leu Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Met Phe Gly Gln Gly Thr
115 120 125
Lys Val Glu Ile Lys Arg Thr
130 135

<210> 36
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 36
Leu Leu Ala Val Ala Pro Gly Ala His Ser Gln Val Gln Leu Val Gln
1 5 10 15
Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
20 25 30
Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Tyr Met His Trp Val Arg

35	40	45													
Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Ile	Ile	Asn	Pro	Ser
50	55	60													
Gly	Asn	Ser	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Met
65	70	75	80												
Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	Ser	Leu
85	90	95													
Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Glu	Lys	Leu	Ala
100	105	110													
Thr	Thr	Ile	Phe	Gly	Val	Leu	Ile	Ile	Thr	Gly	Met	Asp	Tyr	Trp	Gly
115	120	125													
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ser	Ala	Ser	Ala		
130	135	140													

<210> 37
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 37
tgacatttgt atgacccaat ctccagattc ttggctgtg tctctaggtg agagggccac 60
catcaactgc aaggcc 76

<210> 38
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 38
tgaactggta tcaacagaaa ccagggacag 29

<210> 39
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 39
agagtctggg gtccca gacaca ggtttagt 28

<210> 40
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 40
gtcttcagga ccctccgacg ttcgggtggag gtacccaagct gg 42
<210> 41
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 41
caccctcacc atcagttctc tgcaggcgga ggatgttgca gtctatttagt gt 52
<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 42
agctttacag ttactgagca caca 24
<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 43
tcgatgttg ctcagtaact gtaa 24
<210> 44
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 44
ggttcagctg gtgcagtcg gagctgaagt gaagaaggct ggggcttcag tgaagggtgc 60
ctgttaaggt tctgg 75
<210> 45
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 45
agctgggtga ggcaggcacc tggacagggc cttgagtgga tgggagagat tt 52

<210> 46
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 46
caagggcagg gtcacaatga ctagagacac atccaccagc acagtctaca tggaactcag 60

<210> 47
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 47
cagcctgagg tctgaggaca ctgcggctca ttactgtgca aga 43

<210> 48
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 48
gccaaaggac actagtcaact gtgt 24

<210> 49
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 49
actctaaccac tggatggat ctggatcttt ctcctcatc 39

<210> 50
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 50
tcactgccta tgttataagc tgggtgaggc aggcacctg 39

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 51
actagtcaca gtctcctcag c 21

<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 52
gaattcattt acccggagac ag 22

<210> 53
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 53
ccgtgcccag cacctgaact cgccggggca ccgtcgtt tcctcccc 49

<210> 54
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 54
ggtaccaagg tggaaatcaa acgaac 26

<210> 55
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 55
aagcttctaa cactctcccc tgttg 25

<210> 56
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 56
aagcttatgg aatggatctg gatctttctc ctcatcctgt caggaactcg aggtgtccag 60
tcccagggttcc agctgggtg 78

<210> 57
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 57
ctgttaggtcttggataca cattcactgc ctatgttata agctgggtga ggcaggcacc 60
tggacaggccttg 74

<210> 58
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 58
ggtagtagttt attataatga gaagtcaag ggcagggtca caatgactag agacacatcc 60
accagcacag 70

<210> 59
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 59
gaggacactg cggcttattatcttgcaga tccggggacg gcagtcgggtt tgtttactgg 60
ggccaagggtt cactgtt 77

<210> 60
<211> 90
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 60

gtgtatccag aagccttaca ggacaccttc actgaagccc caggcttctt cacttcagct 60
ccagactgca ccagctgaac ctgggactgg 90

<210> 61

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 61

cttctcatta taataactac taccgcttcc aggataaaatc tctcccatcc actcaaggcc 60
ctgtccaggc gcctgcc 77

<210> 62

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 62

gtaatagacc gcagtgcttcc cagacacctag gctgctgagt tccatgtaga ctgtgctgg 60
ggatgtgtct c 71

<210> 63

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 63

gaattcatgg agacagacac aatcctgcta tgggtgctgc tgctctgggt tccaggctcc 60
actggtgac 69

<210> 64

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 64

ggctgtgtct ctaggtgaga gggccaccat caactgcaag gccagccaaa gtgttgatta 60
tgatgg 66

<210> 65

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 65

cagaaaccag gacagccacc caaactcctc atctatgttg catccaatct agagtctggg 60
gtccc 65

<210> 66

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 66

ggacagactt caccctcacc atcagttctc tgcaggcgga ggatgttgca gtctattact 60
gtcagc 66

<210> 67

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 67

cacctagaga cacagccaaa gaatctggag attgggtcat cacaatgtca ccagtggagc 60
ctggaac 67

<210> 68

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 68

ggtggctgtc ctggttctg ttgataccag ttcataatac tatcaccatc ataatcaaca 60
ctttgg 66

<210> 69

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 69

ggtgagggtg aagtctgtcc cagaccact gccactaaac ctgtctggga cccagactc 60
tagattg 67

<210> 70

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 70

ggtacacctca ccgaacgtcg gagggtcctg aagacttgc tgacagtaat agactgcaac 60